



PCT09

## RAW SEQUENCE LISTING

DATE: 01/22/2002

PATENT APPLICATION: US/09/869,136

TIME: 13:24:46

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3 <110> APPLICANT: FRASER, JOHN DAVID
4   PROFT, THOMAS
6 <120> TITLE OF INVENTION: SUPERANTIGENS
8 <130> FILE REFERENCE: 3911-8
10 <140> CURRENT APPLICATION NUMBER: 09/869,136
11 <141> CURRENT FILING DATE: 2001-07-20
13 <150> PRIOR APPLICATION NUMBER: PCT/NZ99/00228
14 <151> PRIOR FILING DATE: 1999-12-24
16 <150> PRIOR APPLICATION NUMBER: NZ 333589
17 <151> PRIOR FILING DATE: 1998-12-24
19 <160> NUMBER OF SEQ ID NOS: 19
21 <170> SOFTWARE: PatentIn Ver. 2.1
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24 <211> LENGTH: 702
25 <212> TYPE: DNA
26 <213> ORGANISM: Streptococcus pyogenes
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35 1 5 10 15
37 ata att tct cgt cct gtg ttt gga tta gaa gta gat aat aat tcc ctt 96
38 Ile Ile Ser Arg Pro Val Phe Gly Leu Glu Val Asp Asn Asn Ser Leu
39 20 25 30
41 cta agg aat atc tat agt acg att gta tat gaa tat tca gat ata gta 144
42 Leu Arg Asn Ile Tyr Ser Thr Ile Val Tyr Glu Tyr Ser Asp Ile Val
43 35 40 45
45 att gat ttt aaa acc agt cat aac tta gtg act aag aaa ctt gat gtt 192
46 Ile Asp Phe Lys Thr Ser His Asn Leu Val Thr Lys Lys Leu Asp Val
47 50 55 60
49 aga gat gct aga gat ttc ttt att aac tcc gaa atg gac gaa tat gca 240
50 Arg Asp Ala Arg Asp Phe Phe Ile Asn Ser Glu Met Asp Glu Tyr Ala
51 65 70 75 80
53 gcc aat gat ttt aaa act gga gat aaa ata gct gtg ttc tcc gtc cca 288
54 Ala Asn Asp Phe Lys Thr Gly Asp Lys Ile Ala Val Phe Ser Val Pro
55 85 90 95
57 ttt gat tgg aac tat tta tca aaa gga aaa gtc aca gca tat acc tat 336
58 Phe Asp Trp Asn Tyr Leu Ser Lys Gly Lys Val Thr Ala Tyr Thr Tyr
59 100 105 110
61 ggt gga ata aca ccc tac caa aaa act tca ata cct aaa aat atc cct 384
62 Gly Gly Ile Thr Pro Tyr Gln Lys Thr Ser Ile Pro Lys Asn Ile Pro

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65 gtt aat tta tgg att aat gga aag cag atc tct gtt cct tac aac gaa 432
66 Val Asn Leu Trp Ile Asn Gly Lys Gln Ile Ser Val Pro Tyr Asn Glu
67          130          135          140
69 ata tca act aac aaa aca aca gtt aca gct caa gaa att gat cta aag 480
70 Ile Ser Thr Asn Lys Thr Thr Val Thr Ala Gln Glu Ile Asp Leu Lys
71 145          150          155          160
73 gtt aga aaa ttt tta ata gca caa cat caa tta tat tct tct ggt tct 528
74 Val Arg Lys Phe Leu Ile Ala Gln His Gln Leu Tyr Ser Ser Gly Ser
75          165          170          175
77 agc tac aaa agt ggt aga ctg gtt ttt cat aca aat gat aat tca gat 576
78 Ser Tyr Lys Ser Gly Arg Leu Val Phe His Thr Asn Asp Asn Ser Asp
79          180          185          190
81 aaa tat tct ttc gat ctt ttc tat gta gga tat aga gat aaa gaa agt 624
82 Lys Tyr Ser Phe Asp Leu Phe Tyr Val Gly Tyr Arg Asp Lys Glu Ser
83          195          200          205
85 atc ttt aaa gta tac aaa gac aat aaa tct ttc aat ata gat aaa att 672
86 Ile Phe Lys Val Tyr Lys Asp Asn Lys Ser Phe Asn Ile Asp Lys Ile
87          210          215          220
89 ggg cat tta gat ata gaa att gac tcc taa 702
90 Gly His Leu Asp Ile Glu Ile Asp Ser
91 225          230
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97 <213> ORGANISM: Streptococcus pyogenes
99 <400> SEQUENCE: 2
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103 Ile Ile Ser Arg Pro Val Phe Gly Leu Glu Val Asp Asn Asn Ser Leu
104          20          25          30
106 Leu Arg Asn Ile Tyr Ser Thr Ile Val Tyr Glu Tyr Ser Asp Ile Val
107          35          40          45
109 Ile Asp Phe Lys Thr Ser His Asn Leu Val Thr Lys Lys Leu Asp Val
110          50          55          60
112 Arg Asp Ala Arg Asp Phe Phe Ile Asn Ser Glu Met Asp Glu Tyr Ala
113 65          70          75          80
115 Ala Asn Asp Phe Lys Thr Gly Asp Lys Ile Ala Val Phe Ser Val Pro
116          85          90          95
118 Phe Asp Trp Asn Tyr Leu Ser Lys Gly Lys Val Thr Ala Tyr Thr Tyr
119          100          105          110
121 Gly Gly Ile Thr Pro Tyr Gln Lys Thr Ser Ile Pro Lys Asn Ile Pro
122          115          120          125
124 Val Asn Leu Trp Ile Asn Gly Lys Gln Ile Ser Val Pro Tyr Asn Glu
125          130          135          140
127 Ile Ser Thr Asn Lys Thr Thr Val Thr Ala Gln Glu Ile Asp Leu Lys
128 145          150          155          160
130 Val Arg Lys Phe Leu Ile Ala Gln His Gln Leu Tyr Ser Ser Gly Ser
131          165          170          175

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133 Ser Tyr Lys Ser Gly Arg Leu Val Phe His Thr Asn Asp Asn Ser Asp
134          180          185          190
136 Lys Tyr Ser Phe Asp Leu Phe Tyr Val Gly Tyr Arg Asp Lys Glu Ser
137          195          200          205
139 Ile Phe Lys Val Tyr Lys Asp Asn Lys Ser Phe Asn Ile Asp Lys Ile
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154 <222> LOCATION: (1)..(702)
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159 1 5 10 15
161 tat gga agt caa tta gct tat gca gat gaa aat tta aaa gat tta aaa 96
162 Tyr Gly Ser Gln Leu Ala Tyr Ala Asp Glu Asn Leu Lys Asp Leu Lys
163 20 25 30
165 aga agt tta aga ttt gcc tat aat att acc cca tgc gat tat gaa aat 144
166 Arg Ser Leu Arg Phe Ala Tyr Asn Ile Thr Pro Cys Asp Tyr Glu Asn
167 35 40 45
169 gta gaa att gca ttt gtt act aca aat agc ata cat att aat act aaa 192
170 Val Glu Ile Ala Phe Val Thr Thr Asn Ser Ile His Ile Asn Thr Lys
171 50 55 60
173 caa aaa aga tcg gaa tgt att ctt tat gtt gat tct att gta tct tta 240
174 Gln Lys Arg Ser Glu Cys Ile Leu Tyr Val Asp Ser Ile Val Ser Leu
175 65 70 75 80
177 ggc att act gat cag ttt ata aaa ggg gat aag gtc gat gtt ttt ggt 288
178 Gly Ile Thr Asp Gln Phe Ile Lys Gly Asp Lys Val Asp Val Phe Gly
179 85 90 95
181 ctc cct tat aat ttt tcc cca cct tat gta gat aat att tat ggt ggt 336
182 Leu Pro Tyr Asn Phe Ser Pro Pro Tyr Val Asp Asn Ile Tyr Gly Gly
183 100 105 110
185 att gta aaa cat tcg aat caa gga aat aaa tca tta cag ttt gta gga 384
186 Ile Val Lys His Ser Asn Gln Gly Asn Lys Ser Leu Gln Phe Val Gly
187 115 120 125
189 att tta aat caa gat ggg aaa gaa act tat ttg ccc tct gag gct gtt 432
190 Ile Leu Asn Gln Asp Gly Lys Glu Thr Tyr Leu Pro Ser Glu Ala Val
191 130 135 140
193 cgc ata aaa aag aaa cag ttt act tta cag gaa ttt gat ttt aaa ata 480
194 Arg Ile Lys Lys Lys Gln Phe Thr Leu Gln Glu Phe Asp Phe Lys Ile
195 145 150 155 160
197 aga aaa ttt cta atg gaa aaa tac aat atc tat gat tcg gaa tcg cgt 528
198 Arg Lys Phe Leu Met Glu Lys Tyr Asn Ile Tyr Asp Ser Glu Ser Arg
199 165 170 175

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201 tat aca tcg ggg agc ctt ttc ctt gct act aaa gat agt aaa cat tat 576
202 Tyr Thr Ser Gly Ser Leu Phe Leu Ala Thr Lys Asp Ser Lys His Tyr
203      180      185      190
205 gaa gtt gat tta ttt aat aag gat gat aag ctt tta agt cga gac agt 624
206 Glu Val Asp Leu Phe Asn Lys Asp Asp Lys Leu Leu Ser Arg Asp Ser
207      195      200      205
209 ttc ttt aaa agg tat aaa gat aat aag att ttt aat agt gaa gaa att 672
210 Phe Phe Lys Arg Tyr Lys Asp Asn Lys Ile Phe Asn Ser Glu Glu Ile
211      210      215      220
213 agt cat ttt gat atc tac tta aaa acg cac tag 705
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215 225      230
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 234
220 <212> TYPE: PRT
221 <213> ORGANISM: Streptococcus pyogenes
223 <400> SEQUENCE: 4
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225 1      5      10      15
227 Tyr Gly Ser Gln Leu Ala Tyr Ala Asp Glu Asn Leu Lys Asp Leu Lys
228      20      25      30
230 Arg Ser Leu Arg Phe Ala Tyr Asn Ile Thr Pro Cys Asp Tyr Glu Asn
231      35      40      45
233 Val Glu Ile Ala Phe Val Thr Thr Asn Ser Ile His Ile Asn Thr Lys
234      50      55      60
236 Gln Lys Arg Ser Glu Cys Ile Leu Tyr Val Asp Ser Ile Val Ser Leu
237 65      70      75      80
239 Gly Ile Thr Asp Gln Phe Ile Lys Gly Asp Lys Val Asp Val Phe Gly
240      85      90      95
242 Leu Pro Tyr Asn Phe Ser Pro Pro Tyr Val Asp Asn Ile Tyr Gly Gly
243      100      105      110
245 Ile Val Lys His Ser Asn Gln Gly Asn Lys Ser Leu Gln Phe Val Gly
246      115      120      125
248 Ile Leu Asn Gln Asp Gly Lys Glu Thr Tyr Leu Pro Ser Glu Ala Val
249      130      135      140
251 Arg Ile Lys Lys Lys Gln Phe Thr Leu Gln Glu Phe Asp Phe Lys Ile
252 145      150      155      160
254 Arg Lys Phe Leu Met Glu Lys Tyr Asn Ile Tyr Asp Ser Glu Ser Arg
255      165      170      175
257 Tyr Thr Ser Gly Ser Leu Phe Leu Ala Thr Lys Asp Ser Lys His Tyr
258      180      185      190
260 Glu Val Asp Leu Phe Asn Lys Asp Asp Lys Leu Leu Ser Arg Asp Ser
261      195      200      205
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285 atg att ata tgt ttg tca ttt ctt tta tat tcc aat gtt gtt caa gca 96
286 Met Ile Ile Cys Leu Ser Phe Leu Leu Tyr Ser Asn Val Val Gln Ala
287 20 25 30
289 aat tct tat aat aca acc aat aga cat aat cta gaa tcg ctt tat aag 144
290 Asn Ser Tyr Asn Thr Thr Asn Arg His Asn Leu Glu Ser Leu Tyr Lys
291 35 40 45
293 cat gat tct aac ttg att gaa gcc gat agt ata aaa aat tct cca gat 192
294 His Asp Ser Asn Leu Ile Glu Ala Asp Ser Ile Lys Asn Ser Pro Asp
295 50 55 60
297 att gta aca agc cat atg ttg aaa tat agt gtc aag gat aaa aat ttg 240
298 Ile Val Thr Ser His Met Leu Lys Tyr Ser Val Lys Asp Lys Asn Leu
299 65 70 75 80
301 tca gtt ttt ttt gag aaa gat tgg ata tca cag gaa ttc aaa gat aaa 288
302 Ser Val Phe Phe Glu Lys Asp Trp Ile Ser Gln Glu Phe Lys Asp Lys
303 85 90 95
305 gaa gta gat att tat gct cta tct gca caa gag gtt tgt gaa tgt cca 336
306 Glu Val Asp Ile Tyr Ala Leu Ser Ala Gln Glu Val Cys Glu Cys Pro
307 100 105 110
309 ggg aaa agg tat gaa gcg ttt ggt gga att aca tta act aat tca gaa 384
310 Gly Lys Arg Tyr Glu Ala Phe Gly Gly Ile Thr Leu Thr Asn Ser Glu
311 115 120 125
313 aaa aaa gaa att aaa gtt cct gta aac gtg tgg gat aaa agt aaa caa 432
314 Lys Lys Glu Ile Lys Val Pro Val Asn Val Trp Asp Lys Ser Lys Gln
315 130 135 140
317 cag ccg cct atg ttt att aca gtc aat aaa ccg aaa gta acc gct cag 480
318 Gln Pro Pro Met Phe Ile Thr Val Asn Lys Pro Lys Val Thr Ala Gln
319 145 150 155 160
321 gaa gtg gat ata aaa gtt aga aag tta ttg att aag aaa tac gat atc 528
322 Glu Val Asp Ile Lys Val Arg Lys Leu Leu Ile Lys Lys Tyr Asp Ile
323 165 170 175
325 tat aat aac cgg gaa caa aaa tac tct aaa gga act gtt acc tta gat 576
326 Tyr Asn Asn Arg Glu Gln Lys Tyr Ser Lys Gly Thr Val Thr Leu Asp
327 180 185 190
329 tta aat tca ggt aaa gat att gtt ttt gat ttg tat tat ttt ggc aat 624
330 Leu Asn Ser Gly Lys Asp Ile Val Phe Asp Leu Tyr Tyr Phe Gly Asn
331 195 200 205
333 gga gac ttt aat agc atg cta aaa ata tat tcc aat aac gag aga ata 672
334 Gly Asp Phe Asn Ser Met Leu Lys Ile Tyr Ser Asn Asn Glu Arg Ile
335 210 215 220
337 gac tca act caa ttt cat gta gat gtg tca atc agc taa 711

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